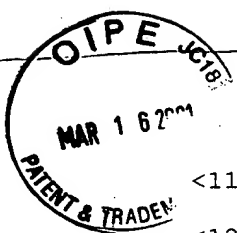


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SEQUENCE LISTING

<110> Bander, Neil H.

<120> TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

<130> Lois M. Kwasigroch: BZL 242/026

<140> US 09/357,709

<141> 1999-07-20

<150> US 08/838,682

<151> 1997-04-09

<150> US 60/016,976

<151> 1996-05-06

<150> US 60/022,125

<151> 1996-07-18

<160> 21

<170> PatentIn version 3.0

<210> 1

<211> 391

<212> DNA

<213> Mus sp.

<400> 1

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catcaatcct aacaatggtg gtaccaccta caatcagaag ttcgaggaca aggccacatt	240
gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga	300
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<211> 391

<212> DNA

<213> Mus sp.

<400> 2

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gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt	180
gtaggtggta ccaccattgt taggattgat gtttccaatc cactcaaggc tctttccatg	240
gctctgcttc acccagtgta tggatatattc agtgaatgtg tatccagaag tcttgagga	300

10560

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tatcctcaact gaag^atcccag gcttcaccag ttcaggtcca gactgttgca gctggacctc 360
agagaggaca cctgcagttc ctagcaggag a 391

<210> 3
<211> 123
<212> PRT
<213> Mus sp.

<400> 3

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Trp	Thr	Thr	Gly	Glu	Ala	Trp	Asp	Phe	Ser	Glu	Asp	Ile	Leu	Gln	Asp
			20					25					30		
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro
		35					40					45			
Trp	Lys	Glu	Pro	Val	Asp	Trp	Lys	His	Gln	Ser	Gln	Trp	Trp	Tyr	His
	50					55					60				
Leu	Gln	Ser	Glu	Val	Arg	Gly	Gln	Gly	His	Ile	Asp	Cys	Arg	Gln	Val
65					70					75					80
Leu	Gln	Tyr	Ser	Leu	His	Gly	Ala	Pro	Gln	Pro	Asn	Ile	Gly	Phe	Cys
				85					90					95	
Ser	Leu	Leu	Leu	Cys	Ser	Trp	Leu	Glu	Leu	Leu	Leu	Gly	Pro	Arg	His
			100					105					110		
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<212> PRT
<213> Mus sp.

<400> 4

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			20					25					30		
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Ile	His	Trp	Val	Lys
			35				40					45			
Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Asn	Ile	Asn	Pro	Asn
	50					55					60				
Asn	Gly	Gly	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Glu	Asp	Lys	Ala	Thr	Leu
65					70					75					80
Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu
				85					90					95	

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Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
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Thr Pro
130

<210> 5
<211> 125
<212> PRT
<213> Mus sp.

<400> 5

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Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
115 120 125

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<213> Mus sp.

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catggaaaga gccttgagtg gattggaaac atcaatccta acaatggtgg taccacctac 180
aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac 240
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aactttgact actggggcca aggcaccact ctcacagtct cctca 345

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<211> 345

<212> DNA
<213> Mus sp.

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ggacttgtct acagtcaatg tggccttgct ctcgaacttc tgattgtagg tggtagcacc 180
attgttagga ttgatgtttc caatccactc aaggctcttt ccatggctct gcttcaccca 240
gtgtatggta tattcagtga atgtgtatcc agaagtcttg caggatatcc tcaactgaagt 300
cccaggcttc accagttcag gtccagactg ttgcagctgg acctc 345

<210> 8
<211> 115
<212> PRT
<213> Mus sp.

<400> 8

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1 5 10 15
Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30
Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45
Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
100 105 110
Val Ser Ser
115

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<213> Mus sp.

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tggtatcaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg 180
tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc 240

atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat 300
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 gta 363

<210> 10
 <211> 363
 <212> DNA
 <213> Mus sp.

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 gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggaccccgct 180
 gtaccgggttg gatgccccgt atatcagcag tttaggagac tgctctgggt tctgttgata 240
 ccaggaaaca taagtaacca cattctcact ggccttgacg gtcaaggtga ccctctctcc 300
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<210> 11
 <211> 121
 <212> PRT
 <213> Mus sp.

<400> 11

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 Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser
 20 25 30
 Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln
 35 40 45
 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val
 50 55 60
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
 85 90 95
 Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105 110
 Lys Arg Ala Asp Ala Ala Pro Thr Val
 115 120

<210> 12

<211> 114
<212> PRT
<213> Mus sp.

<400> 12

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30

Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45

Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60

Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80

Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95

Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110

Leu Tyr

BU
h
v
<210> 13
<211> 116
<212> PRT
<213> Mus sp.

<400> 13

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
1 5 10 15

Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
20 25 30

Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
35 40 45

Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
50 55 60

Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
65 70 75 80

Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
85 90 95

Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
100 105 110

Cys Thr Asn Cys
115

<210> 14
 <211> 321
 <212> DNA
 <213> Mus sp.

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 gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
 cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
 gaagaccttg cagattatca ctgtggacag gggtacagct atccgtacac gttcggaggg 300
 gggaccaagc tggaaataaa a 321

<210> 15
 <211> 321
 <212> DNA
 <213> Mus sp.

<400> 15
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 agatccactg cctgtgaagc gatcggggac cccagtgtac cggttggatg ccccgatat 180
 cagcagttta ggagactgct ctggtttctg ttgataccag gaaacataag taaccacatt 240
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<210> 16
 <211> 107
 <212> PRT
 <213> Mus sp.

<400> 16

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
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 Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 17
<211> 321
<212> DNA
<213> Mus sp.

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ggacaatctc ctaaactact gatttattgg gcatccactc ggcacactgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagac ttcactctca ccattactaa tgttcagtct 240
gaagacttgg cagattatatt ctgtcagcaa tataacagct atcctctcac gttcgggtgct 300
gggaccatgc tggacctgaa a 321

<210> 18
<211> 321
<212> DNA
<213> Mus sp.

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agatccactg cctgtgaagc gatcaggggac tccagtgtgc cgagtggatg cccaataaat 180
cagtagttta ggagattgtc ctggtttctg ttgataccag tctacagcag taccacatc 240
ttgactggcc ttacagatga tgctgaccct gtctcctact gatgtggaca tgaatttgtg 300
agactgggtc atcacaatgt c 321

<210> 19
<211> 107
<212> PRT
<213> Mus sp.

<400> 19

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30
Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
100 105

<210> 20
<211> 125
<212> PRT
<213> Mus sp.

<400> 20

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Asn Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp
35 40 45

Ile Gly Asp Ile Asn Pro Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Tyr Tyr Ser Ser Ser Tyr Met Ala Tyr Tyr Ala Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 21
<211> 109
<212> PRT
<213> Mus sp.

<400> 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu

65

70

75

80

BLV
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
85 90 95

Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105
